

# SEQUENCE LISTING

<110> Gurney, Mark E.  
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 Parodi, Luis A.  
 Yan, Riqiang  
 Pharmacia & Upjohn Company

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Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
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Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
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Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
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Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
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Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
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Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
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Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
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Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr

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 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
 180 185 190  
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro  
 195 200 205  
 Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
 210 215 220  
 Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
 225 230 235 240  
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
 245 250 255  
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
 260 265 270  
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
 275 280 285  
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
 290 295 300  
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
 305 310 315 320  
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
 325 330 335  
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
 340 345 350  
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
 370 375 380  
 Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
 385 390 395 400  
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
 405 410 415  
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
 420 425 430  
 Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
 435 440 445  
 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala  
 450 455 460  
 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp  
 465 470 475 480  
 Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp  
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 Ile Ser Leu Leu Lys  
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<210> 9  
 <211> 2088  
 <212> DNA  
 <213> Homo sapiens

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 atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
 aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagtccga 540  
 ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600  
 gcggaggagg atgactcgga tgtctgggtg ggccgagcag acacagacta tgcagatggg 660  
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 gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
 ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840  
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 gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960  
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 gtcttgccca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca 1560  
 tctttgaccg aaacgaaaac caccgtggag ctcttccccg tgaatggaga gttcagcctg 1620  
 gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680  
 gaagttgagc ctgttgatgc ccgcctgct gccgaccgag gactgaccac tcgaccaggt 1740

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atcgatcatca ccttgggtgat gctgaagaag aaacagtaca catccattca tcatgggtgtg 1980
gtggagggttg acgccgctgt caccgccagag gagcgccacc tgtccaagat gcagcagaac 2040
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<210> 10  
 <211> 695  
 <212> PRT  
 <213> Homo sapiens

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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
      20              25              30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
      35              40              45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
      50              55              60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
      65              70              75              80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
      85              90              95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
      100             105             110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
      115             120             125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
      130             135             140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
      145             150             155             160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
      165             170             175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
      180             185             190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
      195             200             205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
      210             215             220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
      225             230             235             240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
      245             250             255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
      260             265             270

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Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
 275 280 285  
 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
 290 295 300  
 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
 305 310 315 320  
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
 325 330 335  
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
 340 345 350  
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
 355 360 365  
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
 370 375 380  
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
 385 390 395 400  
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
 405 410 415  
 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
 420 425 430  
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
 435 440 445  
 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
 450 455 460  
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
 465 470 475 480  
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
 485 490 495  
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
 500 505 510  
 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
 515 520 525  
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
 530 535 540  
 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
 545 550 555 560  
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
 565 570 575  
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
 580 585 590  
 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
 595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
 610 615 620  
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
 625 630 635 640  
 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
 645 650 655  
 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
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 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
 675 680 685  
 Phe Phe Glu Gln Met Gln Asn  
 690 695

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 <212> DNA  
 <213> Homo sapiens

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 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180  
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 cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
 ggccgcaagc agtgcagac ccaccccac tttgtgattc cctaccgctg cttagttggt 360  
 gaggttgtaa gtgatgcct tctcgcttct gacaagtgca aattcttaca ccaggagagg 420  
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 aagagtacca acttgcattg ctacggcatg ttgctgccct gcggaattga caagttccga 540  
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<210> 12  
 <211> 695

<212> PRT  
 <213> Homo sapiens

<400> 12

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      20           25           30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
      35           40           45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
      50           55           60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
      65           70           75           80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
      85           90           95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
      100          105          110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
      115          120          125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
      130          135          140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
      145          150          155          160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
      165          170          175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
      180          185          190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
      195          200          205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
      210          215          220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
      225          230          235          240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
      245          250          255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
      260          265          270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
      275          280          285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
      290          295          300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
      305          310          315          320

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Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
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 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
 340 345 350  
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
 355 360 365  
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
 370 375 380  
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
 385 390 395 400  
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
 405 410 415  
 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
 420 425 430  
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
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 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
 450 455 460  
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
 465 470 475 480  
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
 485 490 495  
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
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 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
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 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
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 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
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 565 570 575  
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
 580 585 590  
 Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
 595 600 605  
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
 610 615 620  
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
 625 630 635 640  
 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
 645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
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atcttcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980  
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<210> 14  
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<212> PRT  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
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 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
           50                                  55                                  60  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
   65                                  70                                  75                                  80  
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
                                   85                                  90                                  95  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
                   100                                  105                                  110  
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
           115                                  120                                  125  
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
   130                                  135                                  140  
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
  145                                  150                                  155                                  160  
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
                   165                                  170                                  175  
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
                   180                                  185                                  190  
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
   195                                  200                                  205  
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
  210                                  215                                  220  
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
  225                                  230                                  235                                  240  
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
                   245                                  250                                  255  
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
                   260                                  265                                  270  
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
           275                                  280                                  285  
 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
   290                                  295                                  300  
 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
  305                                  310                                  315                                  320  
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
                   325                                  330                                  335  
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
           340                                  345                                  350  
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
           355                                  360                                  365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
 370 375 380  
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
 385 390 395 400  
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
 405 410 415  
 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
 420 425 430  
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
 435 440 445  
 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
 450 455 460  
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
 465 470 475 480  
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
 485 490 495  
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
 500 505  
 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
 515 520 525  
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
 530 535 540  
 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
 545 550 555 560  
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
 565 570 575  
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
 580 585 590  
 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
 595 600 605  
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
 610 615 620  
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
 625 630 635 640  
 Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
 645 650 655  
 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
 660 665 670  
 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
 675 680 685  
 Phe Phe Glu Gln Met Gln Asn  
 690 695

<210> 15  
 <211> 2094  
 <212> DNA  
 <213> Homo sapiens

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 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
 acctgcattg ataccaagga aggcattcctg cagtattgcc aagaagtcta ccctgaactg 240  
 cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
 ggccgcaagc agtgcaagac ccattccccac tttgtgattc cctaccgctg cttagttggt 360  
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 atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag 480  
 aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga 540  
 ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600  
 gcggaggagg atgactcggg tgtctgggtg ggaggagcag acacagacta tgcagatggg 660  
 agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720  
 gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
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 gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960  
 gagaggcttg aggcacaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020  
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 caggagaaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctgggtggag 1140  
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 tacatcaccg ctctgcaggc tgttctctct cggcctcgct acgtgttcaa tatgctaaag 1260  
 aagtatgtcc gcgcagaaca gaaggacaga cagcacacce taaagcattt cgagcatgtg 1320  
 cgcatgggtg atcccaagaa agccgctcag atccgggtcc aggttatgac acacctccgt 1380  
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 gtcttgacca acatgattag tgaaccaagc atcagttacg gaaacgatgc tctcatgcca 1560  
 tctttgaccg aaacgaaaac caccgtggag ctcttccccg tgaatggaga gttcagcctg 1620  
 gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680  
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 atcgatcatc ccttggtgat gctgaagaag aaacagtaca catccattca tcatgggtgtg 1980  
 gtggagggtg acgccgctgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040  
 ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag 2094

<210> 16  
 <211> 697  
 <212> PRT  
 <213> Homo sapiens

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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45  
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
 100 105 110  
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
 115 120 125  
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
 130 135 140  
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
 145 150 155 160  
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
 165 170 175  
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
 180 185 190  
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
 195 200 205  
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
 210 215 220  
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
 225 230 235 240  
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
 245 250 255  
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
 260 265 270  
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
 275 280 285  
 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
 290 295 300  
 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
 305 310 315 320  
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
 325 330 335  
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
 340 345 350  
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
 355 360 365  
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
 370 375 380  
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
 385 390 395 400  
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
 420 425 430  
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
 435 440 445  
 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
 450 455 460  
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
 465 470 475 480  
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
 485 490 495  
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
 500 505 510  
 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
 515 520 525  
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
 530 535 540  
 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
 545 550 555 560  
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
 565 570 575  
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
 580 585 590  
 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
 595 600 605  
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
 610 615 620  
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
 625 630 635 640  
 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
 645 650 655  
 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
 660 665 670  
 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
 675 680 685  
 Phe Phe Glu Gln Met Gln Asn Lys Lys  
 690 695

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 <211> 2094  
 <212> DNA  
 <213> Homo sapiens

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
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 cagatcacca atgtggtaga agccaaccaa ccagtgaacca tccagaactg gtgcaagcgg 300  
 ggccgcaagc agtgcaagac ccattccccac tttgtgattc cctaccgctg cttagtgtgt 360  
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 atggatgttt gcgaaactca tcttctactgg cacaccgtcg ccaaagagac atgcagttag 480  
 aagagtacca acttgcattg ctacggcatg ttgctgccct gcggaattga caagttccga 540  
 ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600  
 gcggaggagg atgactcgga tgtctgggtg ggccggagcag acacagacta tgcagatggg 660  
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 gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
 cctacgaag aagccacaga gagaaccacc agcattgccca ccaccaccac caccaccaca 840  
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 gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960  
 gagaggcttg aggccaaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020  
 gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080  
 caggagaaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctgggtggag 1140  
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 gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc 1440  
 gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaacta ttcagatgac 1500  
 gtcttgccca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca 1560  
 tctttgaccg aaacgaaaac caccgtggag ctccctcccg tgaatggaga gttcagcctg 1620  
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 gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt 1740  
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 ggttcaaaca aaggtgcaat cattggactc atggtgggag gtgttgtcat agcgacagtg 1920  
 atcgtcatca ccttggatg gctgaagaag aaacagtaca catccattca tcatgggtgtg 1980  
 gtggaggttg acgcccgtgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040  
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<210> 18

<211> 697

<212> PRT

<213> Homo sapiens

<400> 18

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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45  
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 65 70 75 80  
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
 100 105 110  
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255  
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270  
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285  
Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300  
Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320  
Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335  
Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350  
Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365  
Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380  
Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400  
Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415  
Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430  
Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445  
Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
 465 470 475 480  
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
 485 490 495  
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
 500 505 510  
 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
 515 520 525  
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
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 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
 545 550 555 560  
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
 565 570 575  
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
 580 585 590  
 Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
 595 600 605  
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
 610 615 620  
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
 625 630 635 640  
 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
 645 650 655  
 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
 660 665 670  
 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
 675 680 685  
 Phe Phe Glu Gln Met Gln Asn Lys Lys  
 690 695

<210> 19  
 <211> 2094  
 <212> DNA  
 <213> Homo sapiens

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 acctgcattg ataccaagga aggcattcctg cagtattgcc aagaagtcta ccctgaactg 240  
 cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
 ggccgcaagc agtgcaagac ccattccccac tttgtgattc cctaccgctg cttagttggt 360  
 gagtttgtaa gtgatgcctt tctcgttctt gacaagtgca aattcttaca ccaggagagg 420  
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 ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600  
 gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg 660



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ccctacgaag aagccacaga gagaaccacc agcattgccca ccaccaccac caccaccaca 840
gagtcctgtg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt 900
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atcttcatca ctttggtgat gctgaagaag aaacagtaca catccattca tcatgggtgtg 1980
gtggaggttg acgccgtgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag 2094

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<210> 20  
 <211> 697  
 <212> PRT  
 <213> Homo sapiens

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
      35                      40                      45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
      50                      55                      60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
      65                      70                      75                      80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
      85                      90                      95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
      100                      105                      110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
      115                      120                      125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
      130                      135                      140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
      145                      150                      155                      160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
      165                      170                      175

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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
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 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
 195 200 205  
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
 210 215 220  
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
 225 230 235 240  
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
 245 250 255  
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
 260 265 270  
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
 275 280 285  
 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
 290 295 300  
 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
 305 310 315 320  
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
 325 330 335  
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
 340 345 350  
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
 355 360 365  
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
 370 375 380  
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
 385 390 395 400  
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
 405 410 415  
 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
 420 425 430  
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
 435 440 445  
 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
 450 455 460  
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
 465 470 475 480  
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
 485 490 495  
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
 500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
 515 520 525  
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
 530 535 540  
 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
 545 550 555 560  
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
 565 570 575  
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
 580 585 590  
 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
 595 600 605  
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
 610 615 620  
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
 625 630 635 640  
 Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
 645 650 655  
 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
 660 665 670  
 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
 675 680 685  
 Phe Phe Glu Gln Met Gln Asn Lys Lys  
 690 695

<210> 21  
 <211> 1341  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 ctgcccctgc gcagcggcct ggggggccc cccctggggc tgcggctgcc ccgggagacc 120  
 gacgaagagc ccgaggagcc cggccggagg ggcagctttg tggagatggt ggacaacctg 180  
 aggggcaagt cggggcaggg ctactacgtg gagatgaccg tgggcagccc cccgcagacg 240  
 ctcaacatcc tgggtgatac aggcagcagt aactttgcag tgggtgctgc cccccacccc 300  
 ttcctgcata gctactacca gaggcagctg tccagcacat accgggacct ccggaagggt 360  
 gtgtatgtgc cctacaccca gggcaagtgg gaaggggagc tgggcaccga cctggtgaagc 420  
 atcccccatg gcccacacgt cactgtgcgt gccaacattg ctgccatcac tgaatcagac 480  
 aagttcttca tcaacggctc caactgggaa ggcatacctg ggctggccta tgctgagatt 540  
 gccaggcctg acgaactcct ggagccttcc tttgactctc tggtaaagca gaccacacgtt 600  
 cccaacctct tctccctgca cctttgtggt gctggcttcc ccccaacca gtctgaagtg 660  
 ctggcctctg tcggaggagg catgatcatt ggaggtatcg accactcgct gtacacagcg 720  
 agtctctggt atacacccat ccggcgggag tggattatg aggtcatcat tgtgcgggtg 780  
 gagatcaatg gacaggatct gaaaatggac tgcaaggagt acaactatga caagagcatt 840  
 gtggacagtg gcaccaccaa ccttcgtttg cccaagaaag tgtttgaagc tgcagtcaaa 900  
 tccatcaagg cagcctcctc cacggagaag ttccctgatg gtttctggct aggagagcag 960  
 ctggtgtgct ggcaagcagg caccaccctt tggaaacatt tccagtcac ctactctac 1020  
 ctaatgggtg aggttaccaa ccagtccttc cgcataacca tccttccgca gcaataacctg 1080  
 cggccagtgg aagatgtggc cacgtcccaa gacgactgtt acaagtttgc catctcacag 1140  
 tcatccacgg gcactgttat gggagctgtt atcatggagg gcttctacgt tgtctttgat 1200

cgggccccgaa aacgaattgg ctttgctgtc agcgcttgcc atgtgcacga tgagttcagg 1260  
 acggcagcgg tggaaggccc tttgtcacc ttggacatgg aagactgtgg ctacaacatt 1320  
 ccacagacag atgagtcag a 1341

<210> 22  
 <211> 446  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
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 His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu  
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 Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly  
 35 40 45  
 Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser  
 50 55 60  
 Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr  
 65 70 75 80  
 Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala  
 85 90 95  
 Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser  
 100 105 110  
 Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly  
 115 120 125  
 Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly  
 130 135 140  
 Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp  
 145 150 155 160  
 Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala  
 165 170 175  
 Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp  
 180 185 190  
 Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu  
 195 200 205  
 Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val  
 210 215 220  
 Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly  
 225 230 235 240  
 Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile  
 245 250 255  
 Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys  
 260 265 270  
 Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu  
 275 280 285

Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala  
 290 295 300  
 Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln  
 305 310 315 320  
 Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val  
 325 330 335  
 Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile  
 340 345 350  
 Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr  
 355 360 365  
 Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly  
 370 375 380  
 Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp  
 385 390 395 400  
 Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His  
 405 410 415  
 Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp  
 420 425 430  
 Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
 435 440 445

<210> 23  
 <211> 1380  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
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 gggggcgccc ccctggggct gcggctgccc ggggagaccg acgaagagcc cgaggagccc 180  
 ggccggaggg gcagctttgt ggagatggtg gacaacctga ggggcaagtc ggggcagggc 240  
 tactacgtgg agatgaccgt gggcagcccc ccgcagacgc tcaacatcct ggtggataca 300  
 ggacgacgta actttgcagt ggggtgctgcc ccccaccct tctgcatcg ctactaccag 360  
 aggcagctgt ccagcacata ccgggacctc cggaagggtg tgtatgtgcc ctacaccag 420  
 ggcaagtggg aaggggagct gggcaccgac ctggttaagca tcccccatgg cccaacgctc 480  
 actgtgcgtg ccaacattgc tgccatcact gaatcagaca agttcttcat caacggctcc 540  
 aactgggaag gcacccctgg gctggcctat gctgagattg ccaggcctga cgactccctg 600  
 gaccctttct ttgactctct ggtaaagcag acccagcttc ccaacctctt ctccctgcac 660  
 ctttgtgggtg ctggcttccc cctcaaccag tctgaagtgc tggcctctgt cggagggagc 720  
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 cggcgggagt ggtattatga ggtcatcatt gtgcgggtgg agatcaatgg acaggatctg 840  
 aaaatggact gcaaggagta caactatgac aagagcattg tggacagtgg caccaccaac 900  
 cttcgtttgc ccaagaaagt gtttgaagct gcagtcaaat ccatcaaggc agcctcctcc 960  
 acggagaagt tccctgatgg tttctggcta ggagagcagc tgggtgtgctg gcaagcaggc 1020  
 accacccctt ggaacatttt ccagtcacac tcactctacc taatgggtga ggttaccaac 1080  
 cagtccttcc gcacacccat ccttcgcgag caatacctgc ggccagtggg agatgtggcc 1140  
 acgtcccaag acgactgtta caagtttgcc atctcacagt catccacggg cactgttatg 1200  
 ggagctgtta tcatggaggg cttctacgtt gtctttgatc gggcccgaac acgaattggc 1260  
 tttgctgtca gcgcttgcca tgtgcacgat gagttcagga cggcagcggt ggaaggccct 1320  
 tttgtcacct tggacatgga agactgtggc tacaacattc cacagacaga tgagtcatga 1380

<210> 24  
 <211> 459

<212> PRT  
 <213> Homo sapiens

<400> 24

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Met	Thr
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Ile	Ser	Asp	Ser	Pro	Arg	Glu	Gln	Asp	Gly	Ser	Thr	Gln	His	Gly	Ile
			20					25					30		
Arg	Leu	Pro	Leu	Arg	Ser	Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg
		35					40					45			
Leu	Pro	Arg	Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly
	50					55					60				
Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly
65					70					75					80
Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile
				85					90					95	
Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His
			100					105					110		
Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg
		115					120					125			
Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu
	130					135					140				
Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val
145					150					155					160
Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe
				165					170					175	
Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu
			180					185					190		
Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val
		195					200					205			
Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	His	Leu	Cys	Gly	Ala
	210					215					220				
Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser
225					230					235					240
Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp
				245					250					255	
Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg
			260					265					270		
Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn
		275					280					285			
Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro
	290					295					300				
Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser
305					310					315					320

Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys  
 325 330 335  
 Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu  
 340 345 350  
 Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu  
 355 360 365  
 Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp  
 370 375 380  
 Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met  
 385 390 395 400  
 Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg  
 405 410 415  
 Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe  
 420 425 430  
 Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp  
 435 440 445  
 Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
 450 455

<210> 25  
 <211> 1302  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
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 ctgcgtctgc cccgggagac cgacgaagag cccgaggagc cgggccggag gggcagcttt 120  
 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 180  
 gtgggcagcc cccgcagac gctcaacatc ctgggtggata caggcagcag taactttgca 240  
 gtgggtgctg cccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 300  
 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 360  
 ctgggcaccg acctggttaag catcccccat ggcccccaacg tcaactgtgcg tgccaacatt 420  
 gctgccatca ctgaatcaga caagtctctc atcaacggct ccaactggga aggcattcctg 480  
 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 540  
 ctggttaaagc agaccacagt tcccaacctc ttctccctgc acctttgtgg tgetggcttc 600  
 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 660  
 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 720  
 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 780  
 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 840  
 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 900  
 ggtttctggc taggagagca gctgggtgtgc tggcaagcag gcaccacccc ttggaacatt 960  
 ttcccagtc tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1020  
 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1080  
 tacaagtttg ccattctaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1140  
 ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc 1200  
 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1260  
 gaagactgtg gctacaacat tccacagaca gatgagtcac ga 1302

<210> 26  
 <211> 433  
 <212> PRT  
 <213> Homo sapiens

<400> 26

Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly  
 1 5 10 15  
 Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu  
 20 25 30  
 Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg  
 35 40 45  
 Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro  
 50 55 60  
 Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala  
 65 70 75 80  
 Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln  
 85 90 95  
 Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr  
 100 105 110  
 Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile  
 115 120 125  
 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr  
 130 135 140  
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu  
 145 150 155 160  
 Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro  
 165 170 175  
 Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser  
 180 185 190  
 Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu  
 195 200 205  
 Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu  
 210 215 220  
 Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr  
 225 230 235 240  
 Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met  
 245 250 255  
 Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr  
 260 265 270  
 Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser  
 275 280 285  
 Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu  
 290 295 300  
 Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile  
 305 310 315 320  
 Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser  
 325 330 335



Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp  
 340 345 350

Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser  
 355 360 365

Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val  
 370 375 380

Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys  
 385 390 395 400

His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val  
 405 410 415

Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu  
 420 425 430

Ser

<210> 27

<211> 1278

<212> DNA

<213> Homo sapiens

<400> 27

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ggcaagtcgg	ggcagggcta	ctacgtggag	atgaccgtgg	gcagccccc	gcagacgctc	180
aacatcctgg	tggatacagg	cagcagtaac	tttgacgtgg	gtgctgcccc	ccacccttc	240
ctgcatcgct	actaccagag	gcagctgtcc	agcacatacc	gggacctccg	gaaggggtgtg	300
tatgtgccct	acaccaggg	caagtgggaa	ggggagctgg	gcaccgacct	ggtaagcatc	360
ccccatggcc	ccaacgtcac	tgtgcgtgcc	aacattgctg	ccatcactga	atcagacaag	420
ttcttcatca	acggctccaa	ctgggaaggc	atcctggggc	tggcctatgc	tgagattgcc	480
aggcctgacg	actccctgga	gcctttcttt	gactctctgg	taaagcagac	ccacgttccc	540
aacctcttct	ccctgcacct	ttgtggtgct	ggcttcccc	tcaaccagtc	tgaagtgtctg	600
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ctctggtata	cacccatccg	gcgggagtg	tattatgagg	tcattcattgt	gcgggtggag	720
atcaatggac	aggatctgaa	aatggactgc	aaggagtaca	actatgacaa	gagcattgtg	780
gacagtggca	ccaccaacct	tcgtttgccc	aagaaagtgt	ttgaagctgc	agtcaaatacc	840
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gtgtgctggc	aagcaggcac	cacccttgg	aacattttcc	cagtcatctc	actctaccta	960
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gcccgaaaac	gaattggctt	tgctgtcagc	gcttgccatg	tgcacgatga	gttcaggacg	1200
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cagacagatg	agtcatga					1278

<210> 28

<211> 425

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr  
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Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe  
 20 25 30

Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr  
 35 40 45  
 Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val  
 50 55 60  
 Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe  
 65 70 75 80  
 Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu  
 85 90 95  
 Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu  
 100 105 110  
 Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val  
 115 120 125  
 Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn  
 130 135 140  
 Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala  
 145 150 155 160  
 Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln  
 165 170 175  
 Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe  
 180 185 190  
 Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile  
 195 200 205  
 Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr  
 210 215 220  
 Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu  
 225 230 235 240  
 Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp  
 245 250 255  
 Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys  
 260 265 270  
 Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu  
 275 280 285  
 Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln  
 290 295 300  
 Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu  
 305 310 315 320  
 Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln  
 325 330 335  
 Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys  
 340 345 350  
 Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala  
 355 360 365

Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg  
370 375 380

Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr  
385 390 395 400

Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly  
405 410 415

Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
420 425

<210> 29  
<211> 1362  
<212> DNA  
<213> Homo sapiens

<400> 29  
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ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180  
gtggagatgg tggacaacct gaggggcaag tccgggcagg gctactacgt ggagatgacc 240  
gtgggcagcc ccccgagac gctcaacatc ctgggtggata caggcagcag taactttgca 300  
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taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
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gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacacct 540  
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gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtgggtattat 780  
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tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900  
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gtccctgat 960  
ggtttctggc taggagagca gctgggtgtg tggcaagcag gcaccacccc ttggaacatt 1020  
ttcccagtca tctcactcta cctaattgggt gaggttacca accagtctt ccgcatcacc 1080  
atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140  
tacaagtttg ccctctcaca gtcattccac ggcactgtta tgggagctgt tatcatggag 1200  
ggcttctacg ttgtctttga tccggcccga aaacgaattg gctttgctgt cagcgtttgc 1260  
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320  
gaagactgtg gctacaacat tccacagaca gatgagtcac ga 1362

<210> 30  
<211> 453  
<212> PRT  
<213> Homo sapiens

<400> 30  
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15  
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30  
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45  
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60  
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80



Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser  
450

<210> 31  
<211> 1380  
<212> DNA  
<213> Homo sapiens

<400> 31  
atggcccaag ccctgccctg gctcctgctg tggatggggc cgggagtgtt gcctgcccac 60  
ggcaccacag acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctggggg 120  
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180  
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300  
gtgggtgtgt cccccaccc ctctcctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccg acctggttaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt 480  
ggtgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacctctg 540  
gggtggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600  
ctggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgcaggcttc 660  
cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatct 720  
gaccactcgc tgtacacagg cagtctcttg tatacaccca tccggcggga gtgggtattat 780  
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840  
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccagaaga 900  
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960  
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020  
ttcccagtc tctcactcta cctaattggg gaggttacca accagtcctt ccgcatcacc 1080  
atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140  
tacaagtttg ccatctcaca gtcattccac ggcactgtta tgggagctgt tatcatggag 1200  
ggcttctacg ttgtctttga tcggggccga aaacgaattg gctttgctgt cagcgcttgc 1260  
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320  
gaagactgtg gctacaacat tccacagaca gatgagtcac agcagcagca gcagcagtga 1380

<210> 32  
<211> 459  
<212> PRT  
<213> Homo sapiens

<400> 32  
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15  
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30  
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45  
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60  
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80  
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
 100 105 110  
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
 115 120 125  
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
 130 135 140  
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
 145 150 155 160  
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
 165 170 175  
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
 180 185 190  
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
 195 200 205  
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
 210 215 220  
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
 225 230 235 240  
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
 245 250 255  
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
 260 265 270  
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
 275 280 285  
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
 290 295 300  
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
 305 310 315 320  
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
 325 330 335  
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
 340 345 350  
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
 355 360 365  
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
 370 375 380  
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
 385 390 395 400  
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
 405 410 415  
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
 420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser His His His His His His  
450 455

<210> 33  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 33  
Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu  
1 5 10 15

Ser Ser Leu Val Arg His Arg Trp Lys  
20 25

<210> 34  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 34  
Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser  
1 5 10 15

Leu Leu Lys

<210> 35  
<211> 29  
<212> DNA  
<213> Homo sapiens

<400> 35  
gtggatccac ccagcacggc atccggctg 29

<210> 36  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 36  
gaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 37  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 37  
gatcgatgac tatctctgac tctccgcgtg aacaggacg 39

<210> 38  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 38

gatccgtcct gttcacgcgg agagtcagag atagtcac

39

<210> 39

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2

<400> 39

cggcatccgg ctgcccctgc gtagcgggtct ggggtgggtgt ccaactgggtc tgcgtctgcc 60  
ccgggagacc gacgaag 77

<210> 40

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2

<400> 40

cttcgtcggg ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60  
ggggcagccg gatgccg 77

<210> 41

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 41

gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 42

gatccgtcgg tttcgatacc agagtcagc ggagagtcag agatagtcac c 51

<210> 43

<211> 32

<212> DNA

<213> Homo sapiens

<400> 43

aaggatcctt tgtggagatg gtggacaacc tg 32

<210> 44

<211> 36

<212> DNA

<213> Homo sapiens



<400> 44  
 gaaagctttc atgactcatc tgtctgtgga atgttg 36  
  
 <210> 45  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: 6-His tag  
  
 <400> 45  
 gatcgcatca tcaccatcac catg 24  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: 6-His tag  
  
 <400> 46  
 gatccatggt gatggtgatg atgc 24  
  
 <210> 47  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Introduce KK  
 motif  
  
 <400> 47  
 gactgaccac tcgaccaggt tc 22  
  
 <210> 48  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Introduce KK  
 motif  
  
 <400> 48  
 cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51  
  
 <210> 49  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Introduce KK  
 motif  
  
 <400> 49  
 cgaattaaat tccagcacac tggcta 26